

Using MicroArray Explorer with the NCI/CIT mAdb Web server

<http://www.lecb.ncifcrf.gov/MAExplorer>
<http://nciarray.nci.nih.gov/>

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Overview: MAExplorer and mAdb

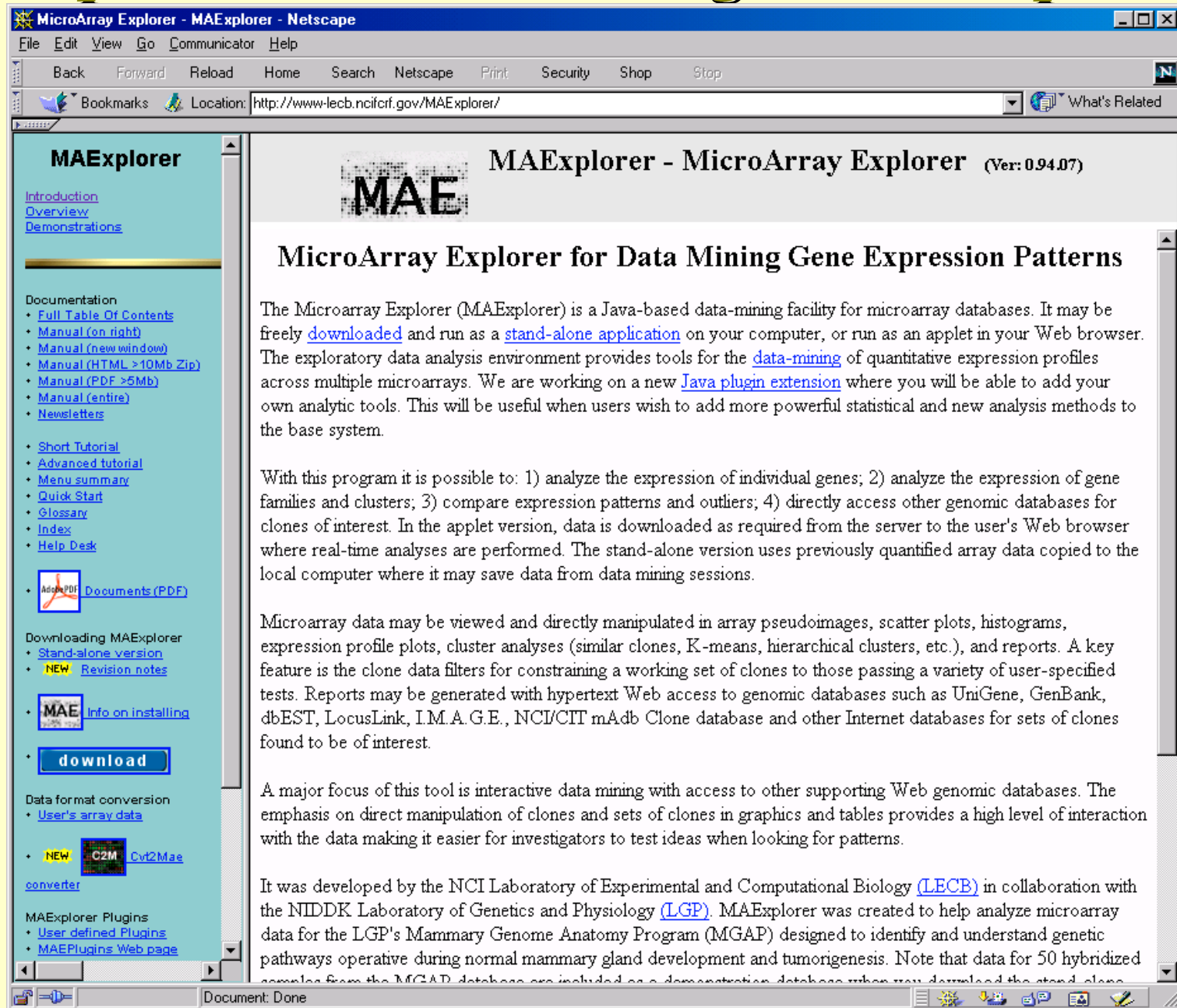
- **MAExplorer** is a Java data-mining tool for analyzing microarrays running on a user's computer. It provides real time response required for data-mining, as well as connecting to Genomic databases such as UniGene, mAdb-clone DB, Genbank, etc. [<http://www.lecb.ncifcrf.gov/MAExplorer>]
- The NCI/CIT **mAdb** Web microarray database server is a data repository, publishing and analysis facility for microarrays created in conjunction with the NCI-ATC facility. [<http://nciarray.nci.nih.gov/>]
- MAExplorer may be used with mAdb data as a stand-alone application on the users computer (Windows 95/98/NT/2000/XP MacOS/-X, Solaris, Linux, Unix).
- It uses a set of data files downloaded, as a Zip file, from the mAdb Web server in a format compatible with MAExplorer.
- This document describes the procedures for downloading 1) MAExplorer, 2) a mAdb data set and 3) starting MAExplorer with that data. MAExplorer is fully documented on its Web site including a reference manual, slide-shows, tutorials and demonstration databases.

1. Procedure to download & install MAExplorer

1. Go to **<http://www.lecb.ncifcrf.gov/MAExplorer>** with your Web browser.
2. Select **Download** to start the install process. It uses the InstallAnywhere™ program to install it on your computer. You have a choice of:
 - 3.1 Allowing InstallAnywhere™ to install it in a standard default location (eg. in Windows this would be C:\Program Files\MAExplorer), or
 - 3.2 You may download the installer file and select where you want to install it.
 - A) Find your computer **Platform** in the list. Click on the corresponding **Download** word and save the installer on your computer.
 - B) Go to **View** for your platform in the same download Web page to see how to finish the installation for your particular platform.
 - C) Now install MAExplorer on your computer in the location you desire.
4. You are ready to use MAExplorer. Eg. in the Windows Start menu, click on MAExplorer. After it starts, select “Open file DB” in the File menu.

1.1 MAExplorer Home Page

<http://www.lecb.ncifcrf.gov/MAExplorer/>




The screenshot shows a Netscape browser window titled "MicroArray Explorer - MAExplorer - Netscape". The address bar displays "http://www.lecb.ncifcrf.gov/MAExplorer/". The page layout includes a left sidebar and a main content area.

MAExplorer


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Documentation


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Downloading MAExplorer

- [Stand-alone version](#)
- **NEW** [Revision notes](#)
-  [Info on installing](#)
- **download**

Data format conversion

- [User's array data](#)
- **NEW**  [Cvt2Mae converter](#)

MAExplorer Plugins

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- [MAEPlugins Web page](#)

MAExplorer - MicroArray Explorer (Ver: 0.94.07)

MicroArray Explorer for Data Mining Gene Expression Patterns

The Microarray Explorer (MAExplorer) is a Java-based data-mining facility for microarray databases. It may be freely [downloaded](#) and run as a [stand-alone application](#) on your computer, or run as an applet in your Web browser. The exploratory data analysis environment provides tools for the [data-mining](#) of quantitative expression profiles across multiple microarrays. We are working on a new [Java plugin extension](#) where you will be able to add your own analytic tools. This will be useful when users wish to add more powerful statistical and new analysis methods to the base system.

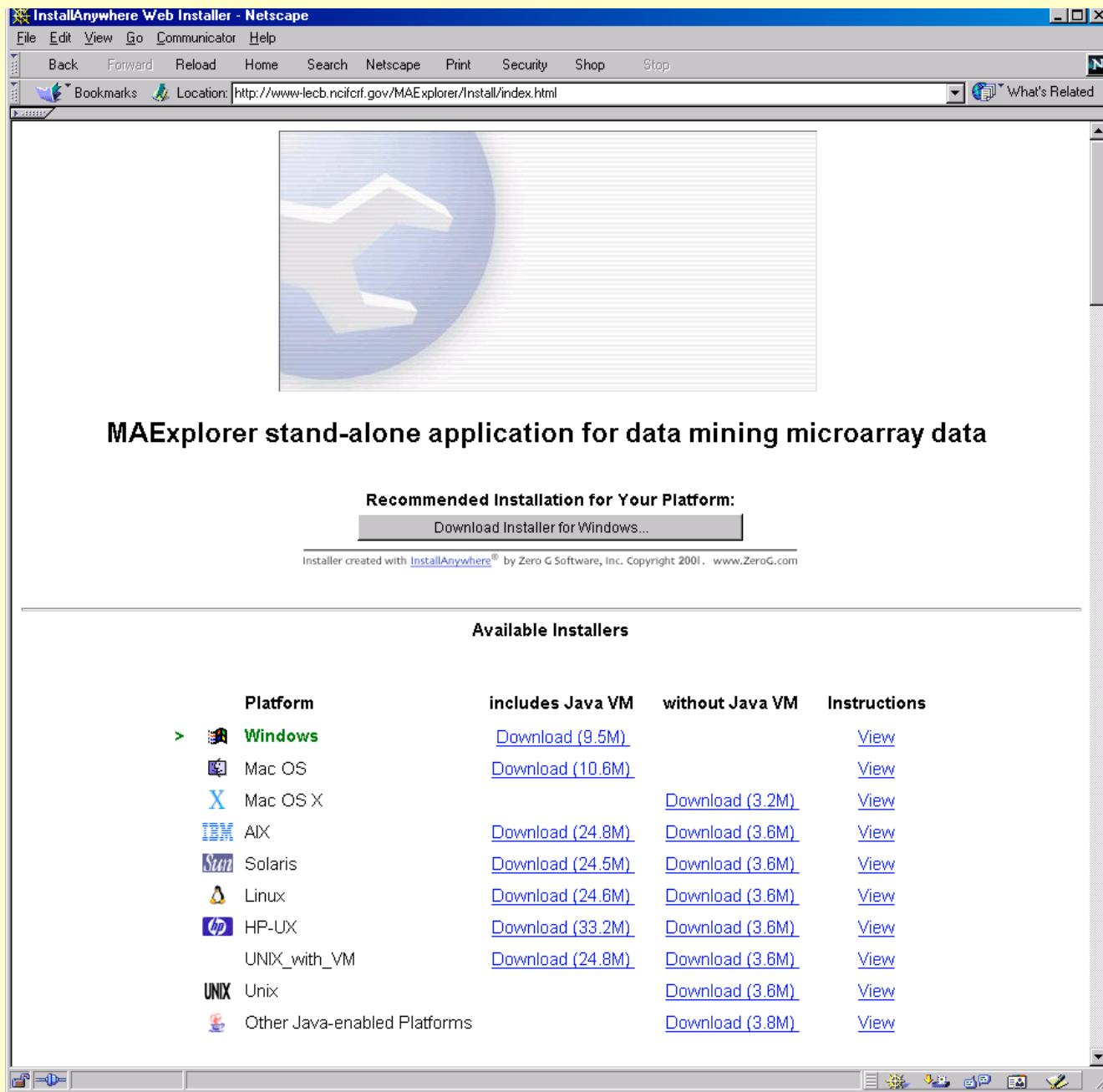
With this program it is possible to: 1) analyze the expression of individual genes; 2) analyze the expression of gene families and clusters; 3) compare expression patterns and outliers; 4) directly access other genomic databases for clones of interest. In the applet version, data is downloaded as required from the server to the user's Web browser where real-time analyses are performed. The stand-alone version uses previously quantified array data copied to the local computer where it may save data from data mining sessions.

Microarray data may be viewed and directly manipulated in array pseudoinages, scatter plots, histograms, expression profile plots, cluster analyses (similar clones, K-means, hierarchical clusters, etc.), and reports. A key feature is the clone data filters for constraining a working set of clones to those passing a variety of user-specified tests. Reports may be generated with hypertext Web access to genomic databases such as UniGene, GenBank, dbEST, LocusLink, I.M.A.G.E., NCI/CIT mAdb Clone database and other Internet databases for sets of clones found to be of interest.

A major focus of this tool is interactive data mining with access to other supporting Web genomic databases. The emphasis on direct manipulation of clones and sets of clones in graphics and tables provides a high level of interaction with the data making it easier for investigators to test ideas when looking for patterns.

It was developed by the NCI Laboratory of Experimental and Computational Biology ([LECB](#)) in collaboration with the NIDDK Laboratory of Genetics and Physiology ([LGP](#)). MAExplorer was created to help analyze microarray data for the LGP's Mammary Genome Anatomy Program (MGAP) designed to identify and understand genetic pathways operative during normal mammary gland development and tumorigenesis. Note that data for 50 hybridized samples from the MGAP database are included as a demonstration database when you download the stand-alone

1.2 Download Stand-alone version Web page - find your “Platform”, then select “Download”




InstallAnywhere Web Installer - Netscape

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Bookmarks Location: <http://www-lecb.ncicrf.gov/MAExplorer/Install/index.html> What's Related



MAExplorer stand-alone application for data mining microarray data

Recommended Installation for Your Platform:

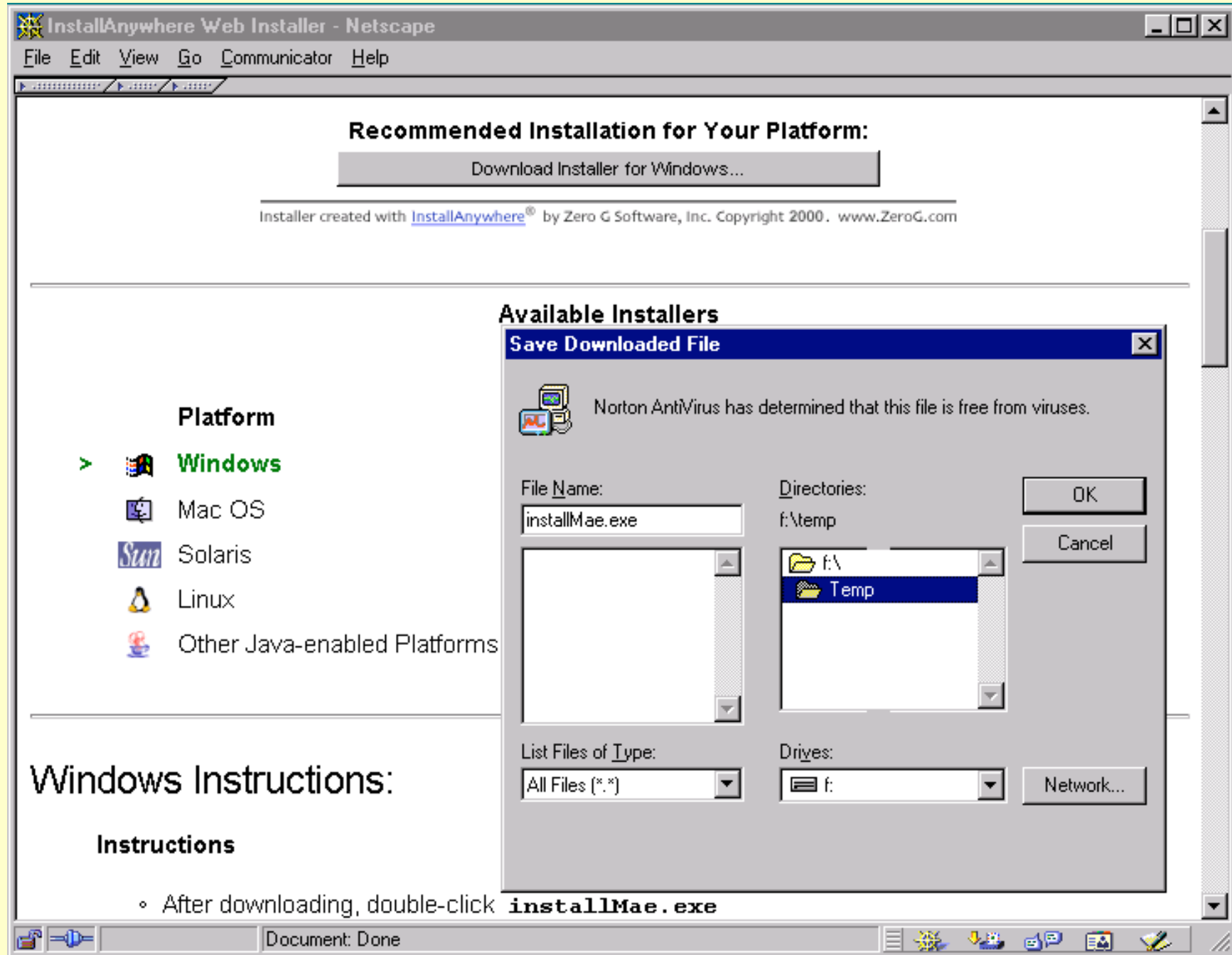
[Download Installer for Windows...](#)

Installer created with [InstallAnywhere](#)® by Zero G Software, Inc. Copyright 2001. www.ZeroG.com

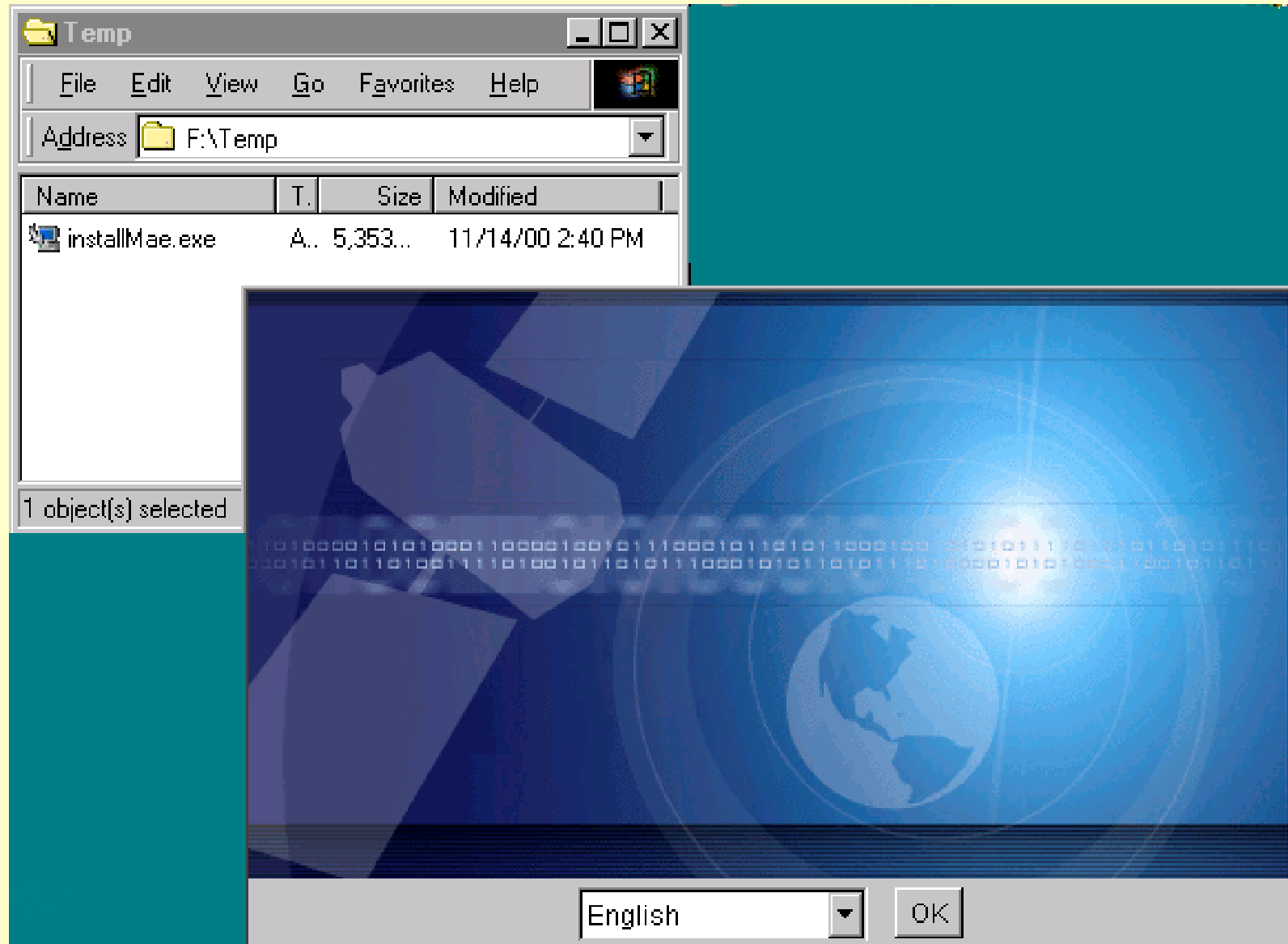
Available Installers

Platform	includes Java VM	without Java VM	Instructions
> Windows	Download (9.5M)		View
Mac OS	Download (10.6M)		View
Mac OS X		Download (3.2M)	View
AIX	Download (24.8M)	Download (3.6M)	View
Solaris	Download (24.5M)	Download (3.6M)	View
Linux	Download (24.6M)	Download (3.6M)	View
HP-UX	Download (33.2M)	Download (3.6M)	View
UNIX_with_VM	Download (24.8M)	Download (3.6M)	View
UNIX Unix		Download (3.6M)	View
Other Java-enabled Platforms		Download (3.8M)	View

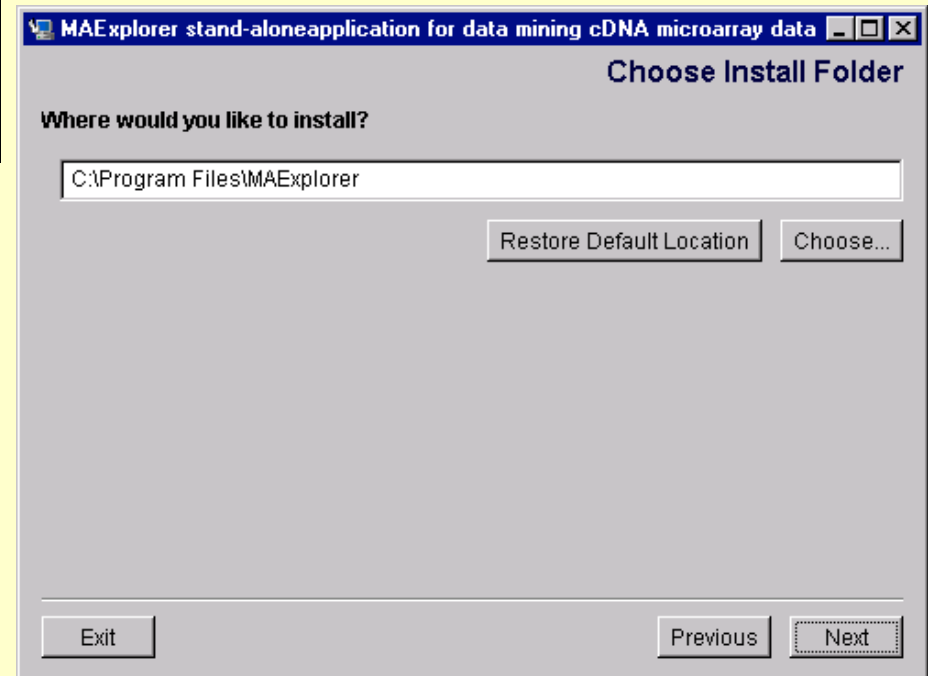
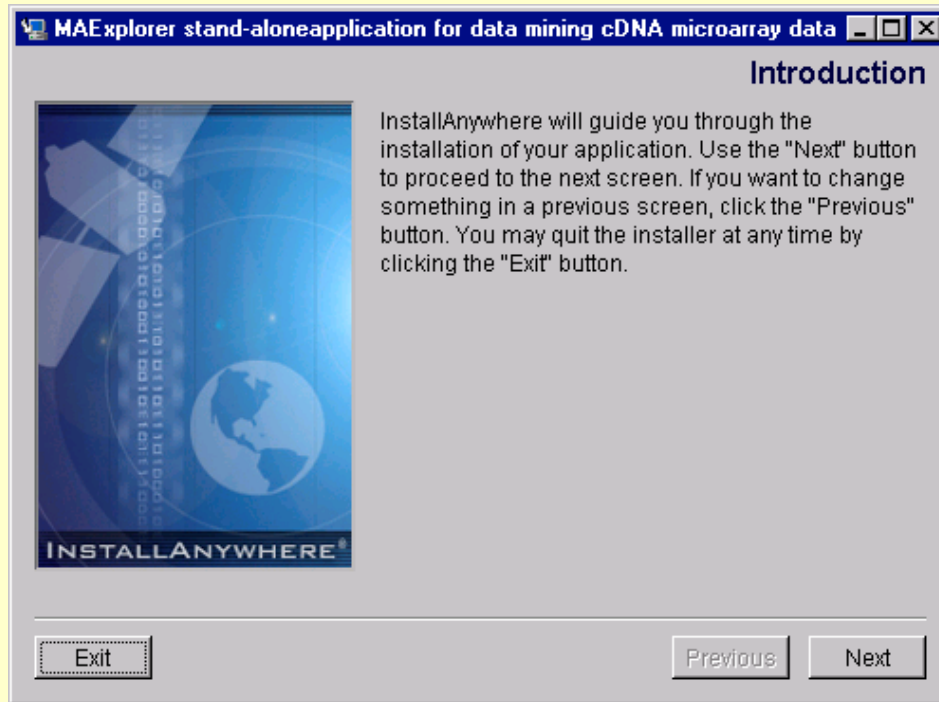
1.3 Save the installer on your local computer



1.4 Start the installer - e.g. in Windows, click on installMAE.exe. Then answer questions, “OK” etc.

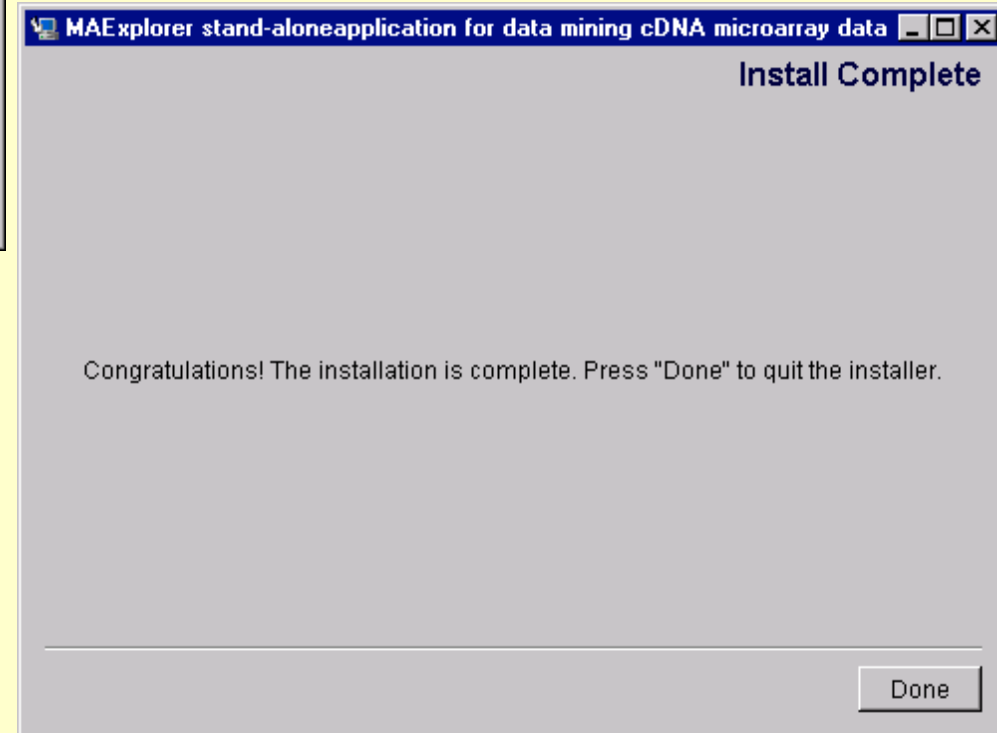
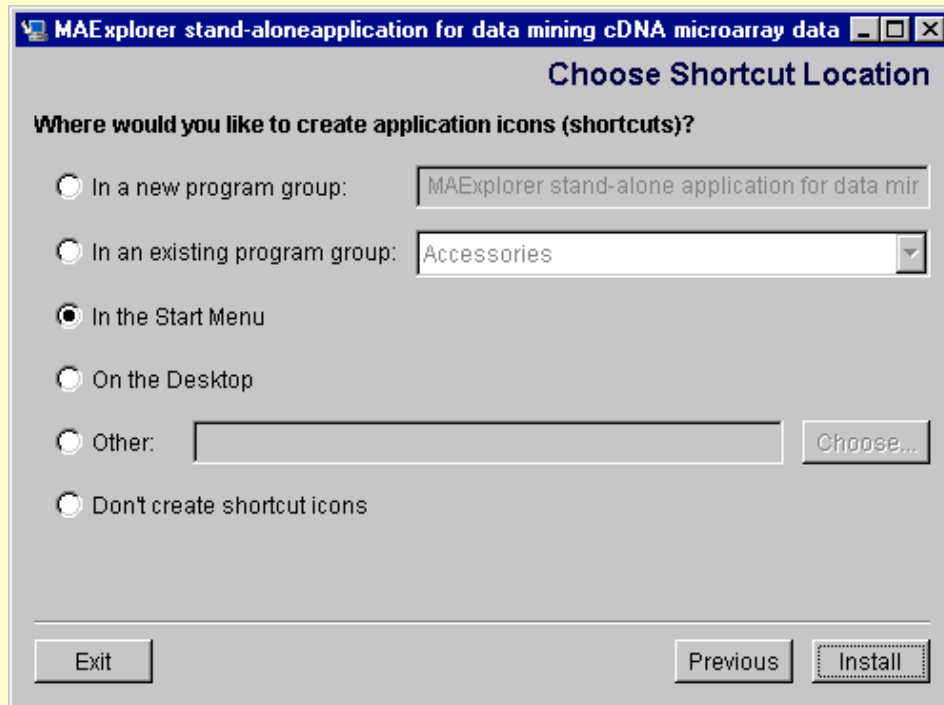


1.5 Successive steps during installation of MAExplorer

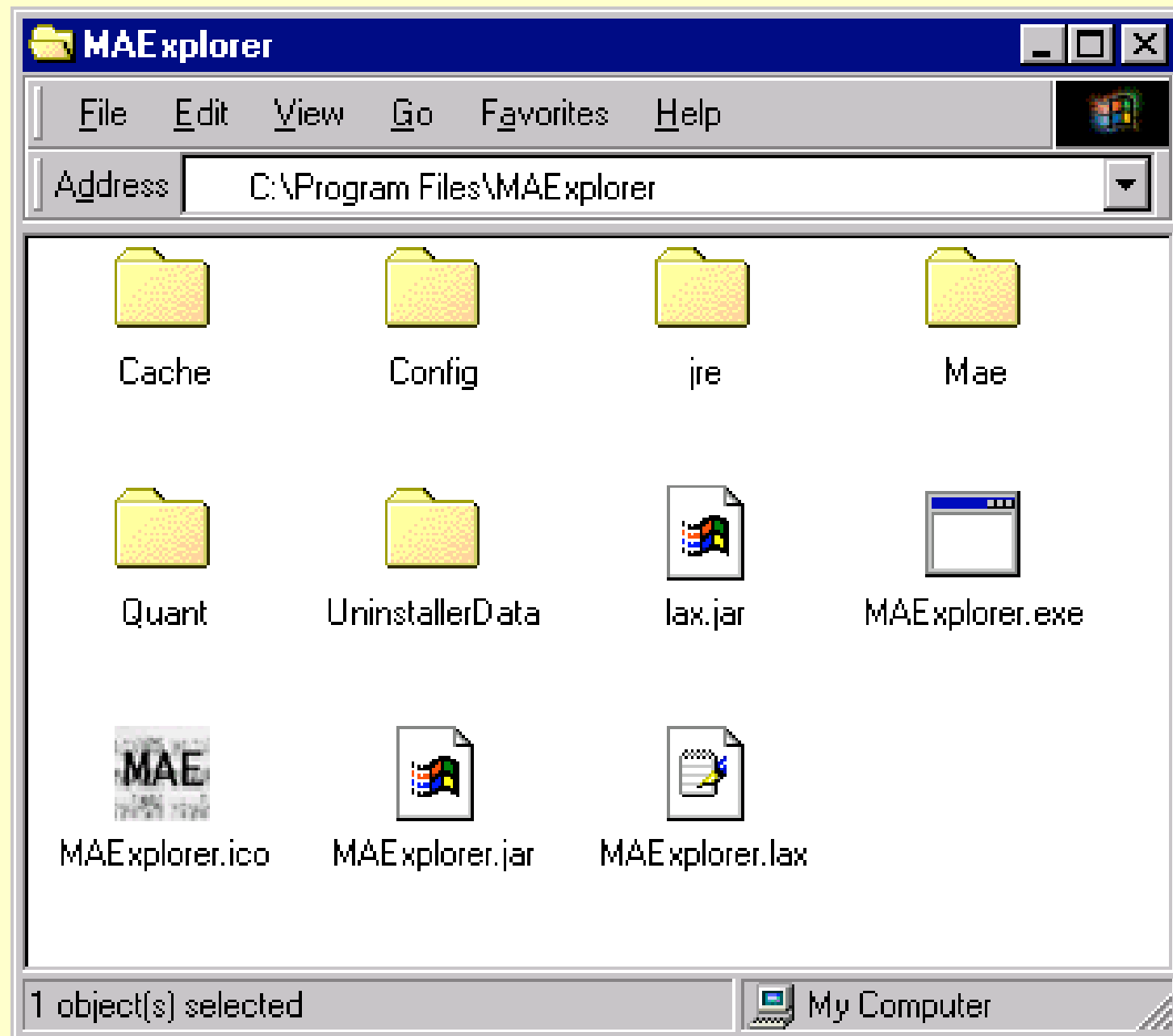


1.6 Finish installation of MAExplorer:

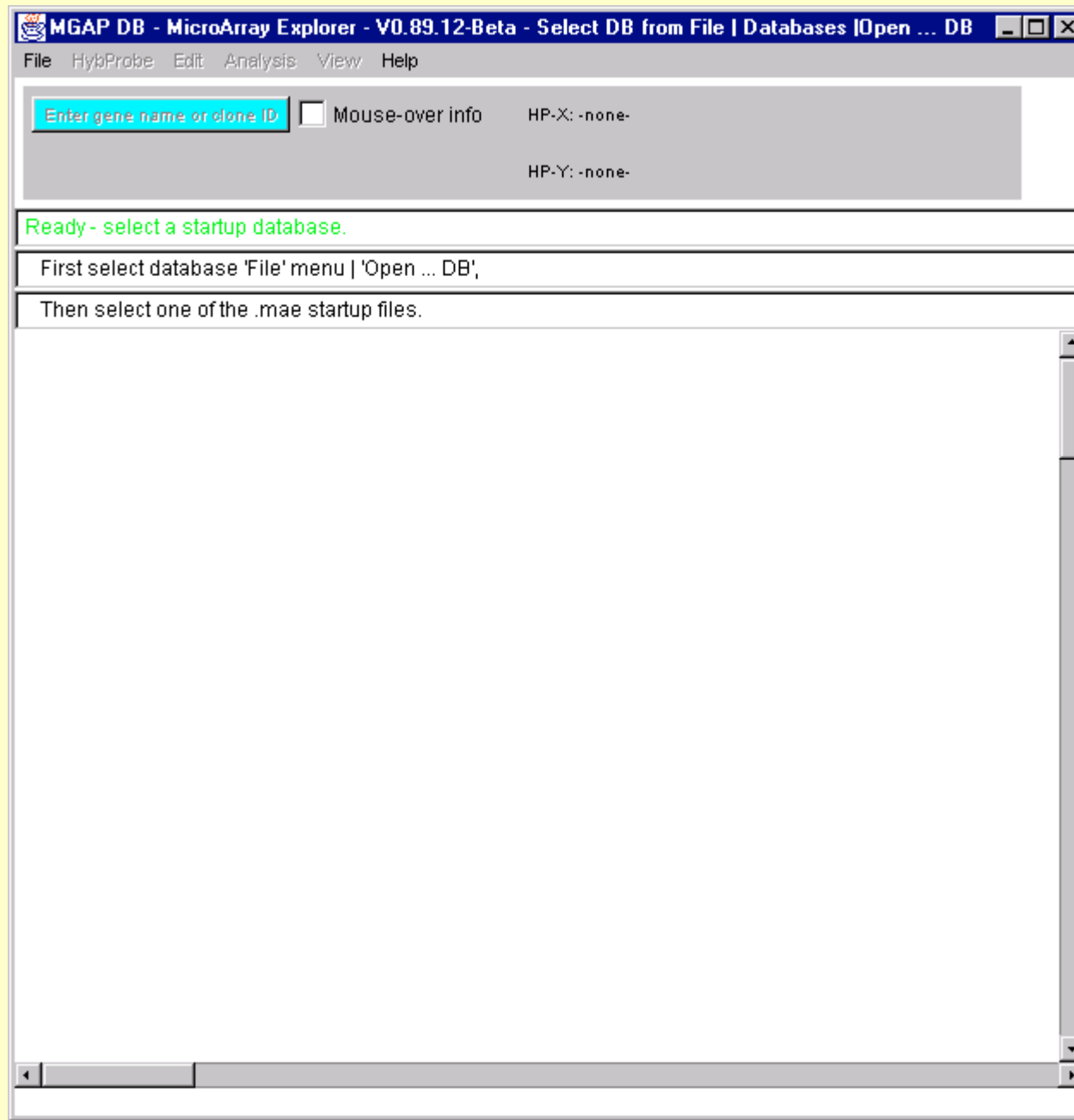
A) press “Install”, B) press “Done”



1.7 Directory structure of downloaded files

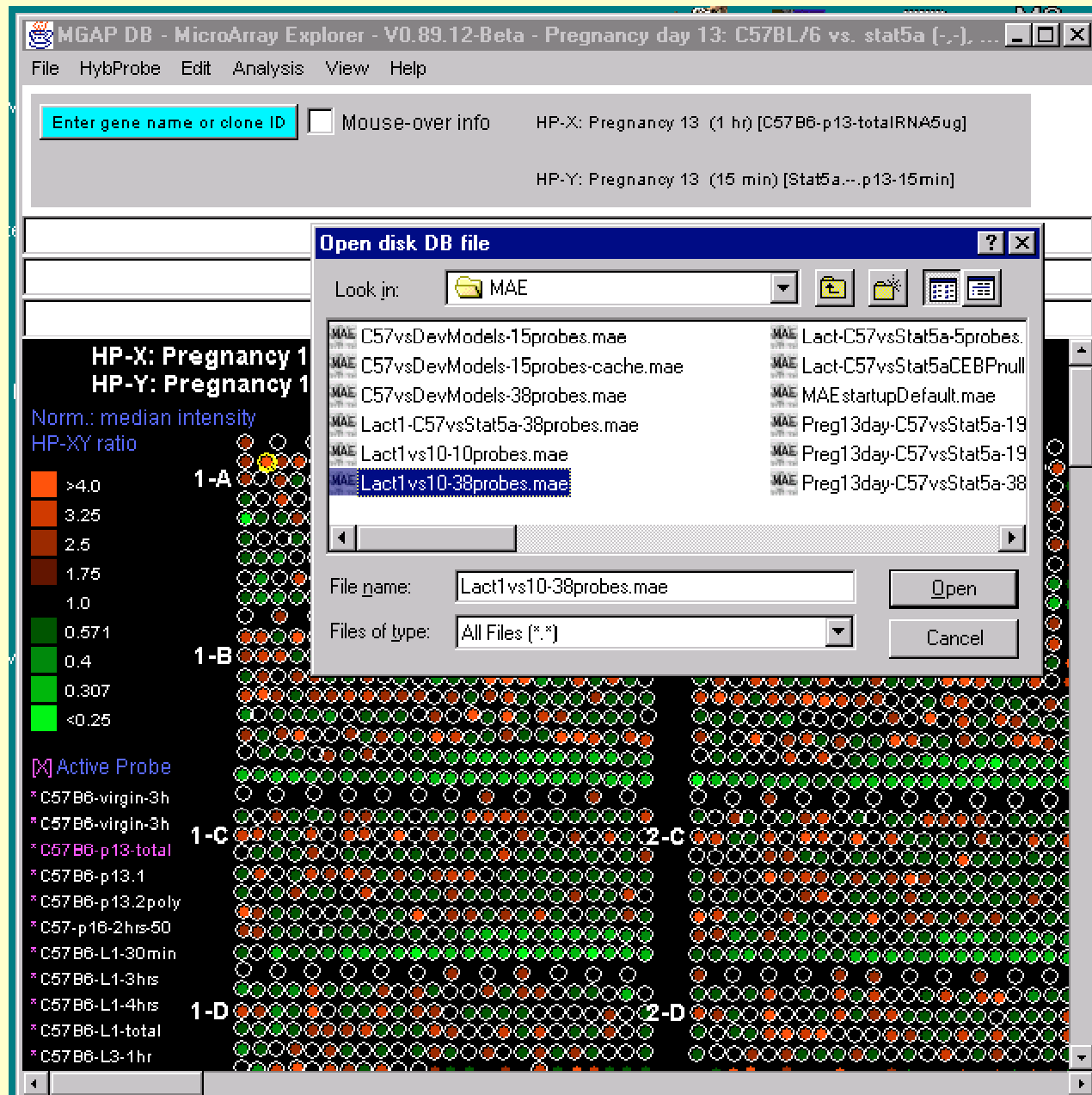


1.8 Start MAExplorer from Windows PC “Start” menu. Initially starts with empty database .



1.9 Open demo (MGAP) database from local disk

Browse demo project for startup database. Select File menu, then Open file DB

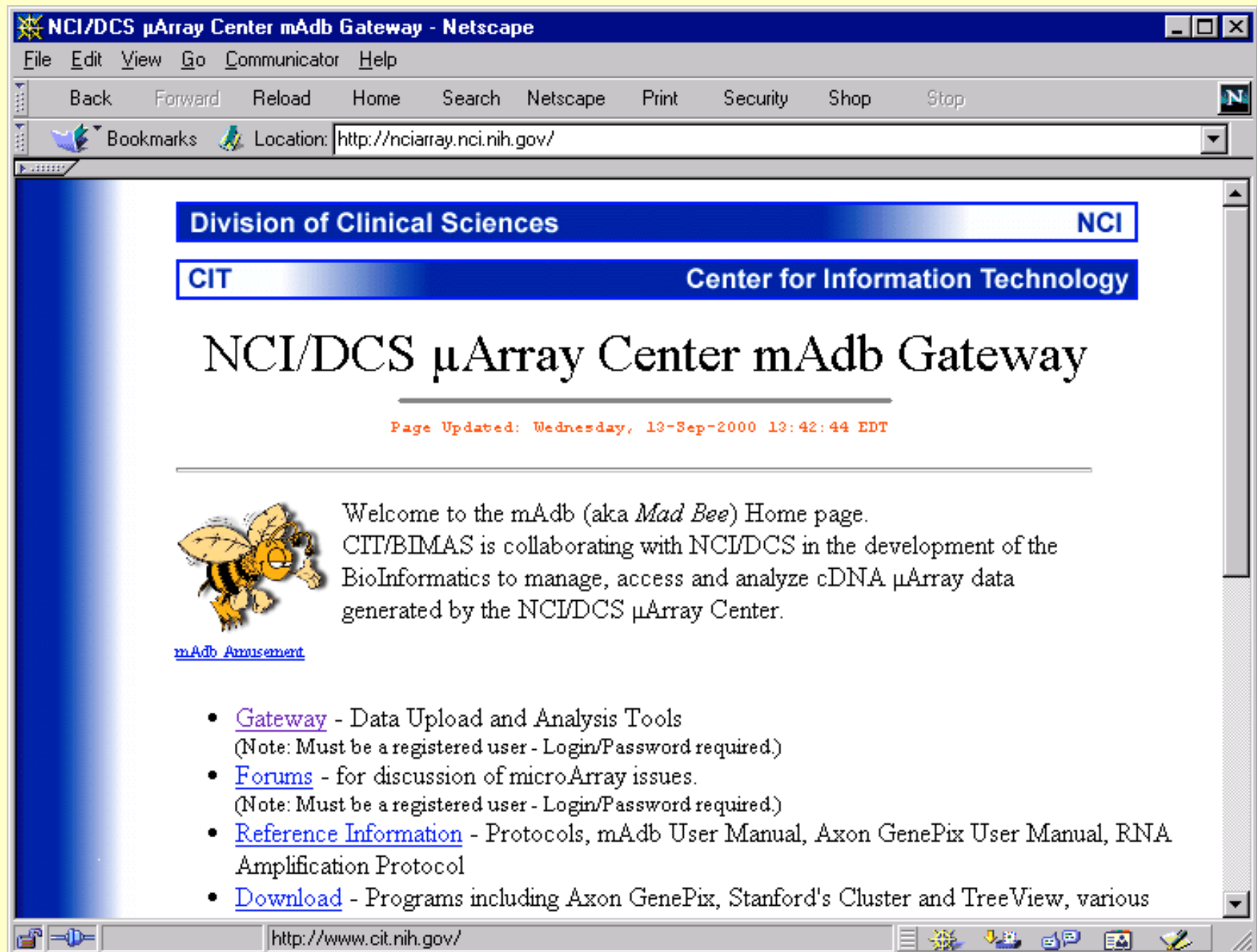


2. Procedure to use MAExplorer on mAdb data

1. Install MAExplorer if not already installed
2. Go to <http://nciarray.nci.nih.gov/> with your Web browser
3. Go to "**Gateway**" and log into your account
4. In "**Projects:**", select projects & samples for export
5. In "**Tool:**", select "**BETA formatted array data retrieval tool**"
6. Select "**LECB/NCI MAExplorer**" for "Retrieval format"
7. **Submit**. This eventually replaces Web page with new page containing numbered file ending in **.zip**
8. Click on **.zip** file to download & save it locally to your disk.
9. Unpack **.zip** file to new directory, for example "**C:\myData**"
10. On Windows systems, double click on Start.mae in **C:\myData\MAE** directory. This will start MAExplorer

2.1 NCI/CIT mAdb Web server home page

<http://nciarray.nci.nih.gov/>



The screenshot shows a Netscape browser window titled "NCI/DCS μArray Center mAdb Gateway - Netscape". The address bar displays "http://nciarray.nci.nih.gov/". The page content includes a blue header with "Division of Clinical Sciences" and "NCI", followed by "CIT" and "Center for Information Technology". The main title is "NCI/DCS μArray Center mAdb Gateway". Below this, a red timestamp reads "Page Updated: Wednesday, 13-Sep-2000 13:42:44 EDT". A cartoon bee character is positioned to the left of the welcome text. The text reads: "Welcome to the mAdb (aka *Mad Bee*) Home page. CIT/BIMAS is collaborating with NCI/DCS in the development of the BioInformatics to manage, access and analyze cDNA μArray data generated by the NCI/DCS μArray Center." Below this is a link "mAdb Amusement". A bulleted list of links is provided: "Gateway" (Data Upload and Analysis Tools, Note: Must be a registered user - Login/Password required.), "Forums" (for discussion of microArray issues, Note: Must be a registered user - Login/Password required.), "Reference Information" (Protocols, mAdb User Manual, Axon GenePix User Manual, RNA Amplification Protocol), and "Download" (Programs including Axon GenePix, Stanford's Cluster and TreeView, various). The status bar at the bottom shows "http://www.cit.nih.gov/".

NCI/DCS μArray Center mAdb Gateway - Netscape

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Bookmarks Location: <http://nciarray.nci.nih.gov/>

Division of Clinical Sciences NCI

CIT Center for Information Technology

NCI/DCS μArray Center mAdb Gateway

Page Updated: Wednesday, 13-Sep-2000 13:42:44 EDT

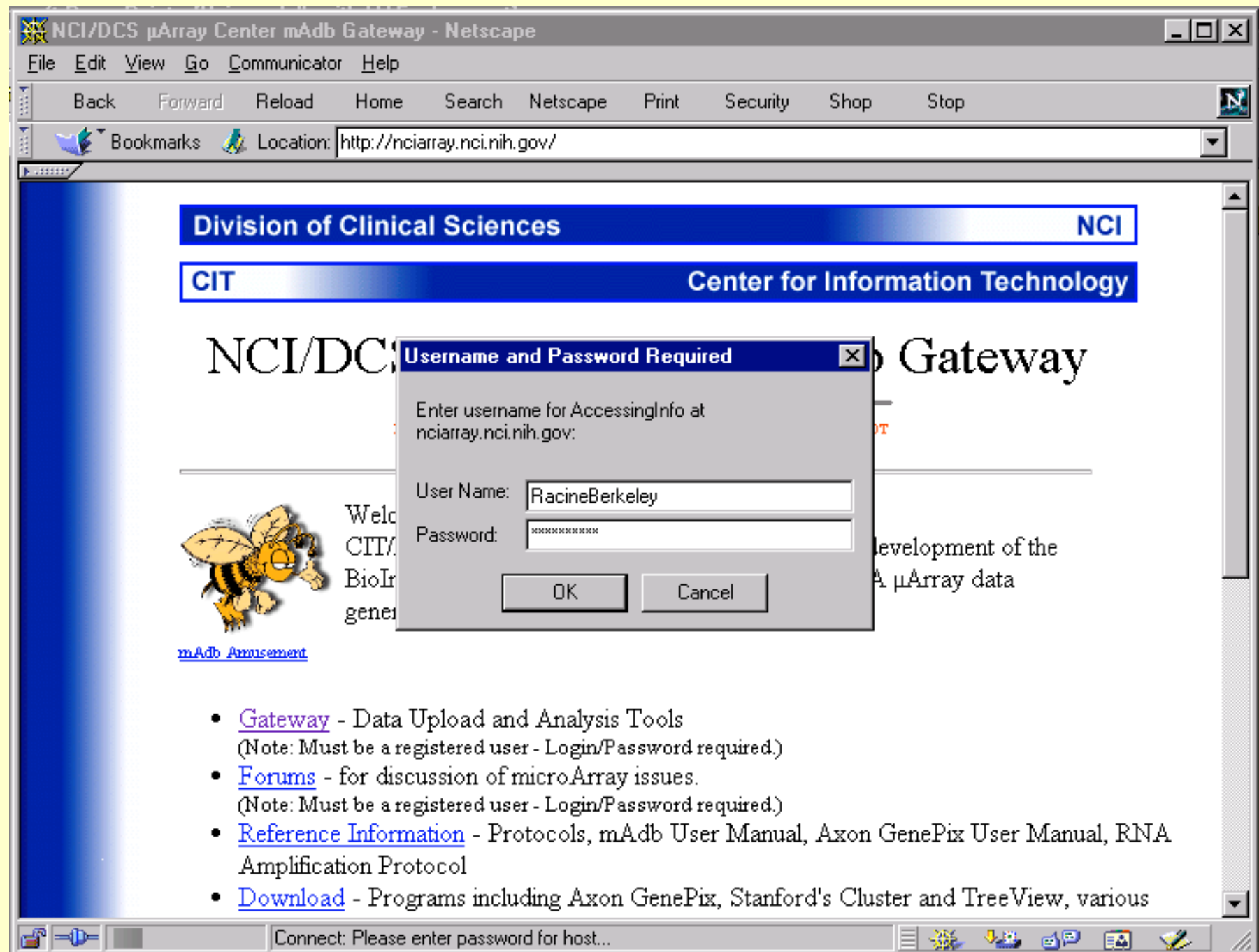
 Welcome to the mAdb (aka *Mad Bee*) Home page.
CIT/BIMAS is collaborating with NCI/DCS in the development of the BioInformatics to manage, access and analyze cDNA μArray data generated by the NCI/DCS μArray Center.

[mAdb Amusement](#)

- [Gateway](#) - Data Upload and Analysis Tools
(Note: Must be a registered user - Login/Password required.)
- [Forums](#) - for discussion of microArray issues.
(Note: Must be a registered user - Login/Password required.)
- [Reference Information](#) - Protocols, mAdb User Manual, Axon GenePix User Manual, RNA Amplification Protocol
- [Download](#) - Programs including Axon GenePix, Stanford's Cluster and TreeView, various

<http://www.cit.nih.gov/>

2.2 Press “Gateway” & Log on to the mAdb server



NCI/DCS μ Array Center mAdb Gateway - Netscape

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Bookmarks Location: <http://nciarray.nci.nih.gov/>

Division of Clinical Sciences NCI

CIT Center for Information Technology

NCI/DCS μ Array Gateway

Enter username for AccessingInfo at nciarray.nci.nih.gov:

User Name:

Password:

OK Cancel

WELCOME
CIT/NCI
BioIn
genes

[mAdb Amusement](#)

- [Gateway](#) - Data Upload and Analysis Tools
(Note: Must be a registered user - Login/Password required.)
- [Forums](#) - for discussion of microArray issues.
(Note: Must be a registered user - Login/Password required.)
- [Reference Information](#) - Protocols, mAdb User Manual, Axon GenePix User Manual, RNA Amplification Protocol
- [Download](#) - Programs including Axon GenePix, Stanford's Cluster and TreeView, various

Connect: Please enter password for host...

2.3 Select: a) Projects, b) “Formatted Array data Retrieval Tool”, c) then press “Continue”

The screenshot shows a Netscape browser window titled "mArray Tools - Netscape". The address bar displays the URL "http://nciararray.nci.nih.gov/cgi-bin/restricted/beta/cgi-bin/MAAccessTools.pl". The page header includes "Division of Clinical Sciences" and "NCI" on the right, and "CIT" and "Center for Information Technology" on the left. The main heading is "Top Level Analysis Selection". Below this, it says "Choose one or more Projects, Analysis Tool and then Continue". A note states: "Note: Tools marked with '*' only support selection of one project". Under the "Projects:" label, there is a list box containing two items: "quest - Time Course Demo Set #1" and "quest - Repeats and Reciprocal Retests Demo Set #3". Under the "Tool:" label, there is a dropdown menu currently showing "BETA Formatted Array Data Retrieval Tool". At the bottom of the form is a "Continue" button. The browser's status bar at the bottom shows "Document: Done".

mArray Tools - Netscape

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Bookmarks Location: <http://nciararray.nci.nih.gov/cgi-bin/restricted/beta/cgi-bin/MAAccessTools.pl>

Division of Clinical Sciences NCI

CIT Center for Information Technology

Top Level Analysis Selection

Choose one or more Projects, Analysis Tool and then Continue

Note: Tools marked with "*" only support selection of one project

Projects:

- quest - Time Course Demo Set #1
- quest - Repeats and Reciprocal Retests Demo Set #3

Tool: BETA Formatted Array Data Retrieval Tool

Continue

Document: Done

2.4 Set a) Format option to “MAExplorer”, b) select arrays to be analyzed, c) press “Submit”

Data Retrieval Form - Netscape

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Bookmarks Location: ciarray.nci.nih.gov/cgi-bin/restricted/mAdb_formatted_dataretrieval_form_v1.cgi?project=109&project=111


Division of Clinical Sciences **NCI**

CIT **Center for Information Technology**

mAdb: Data Retrieval Form

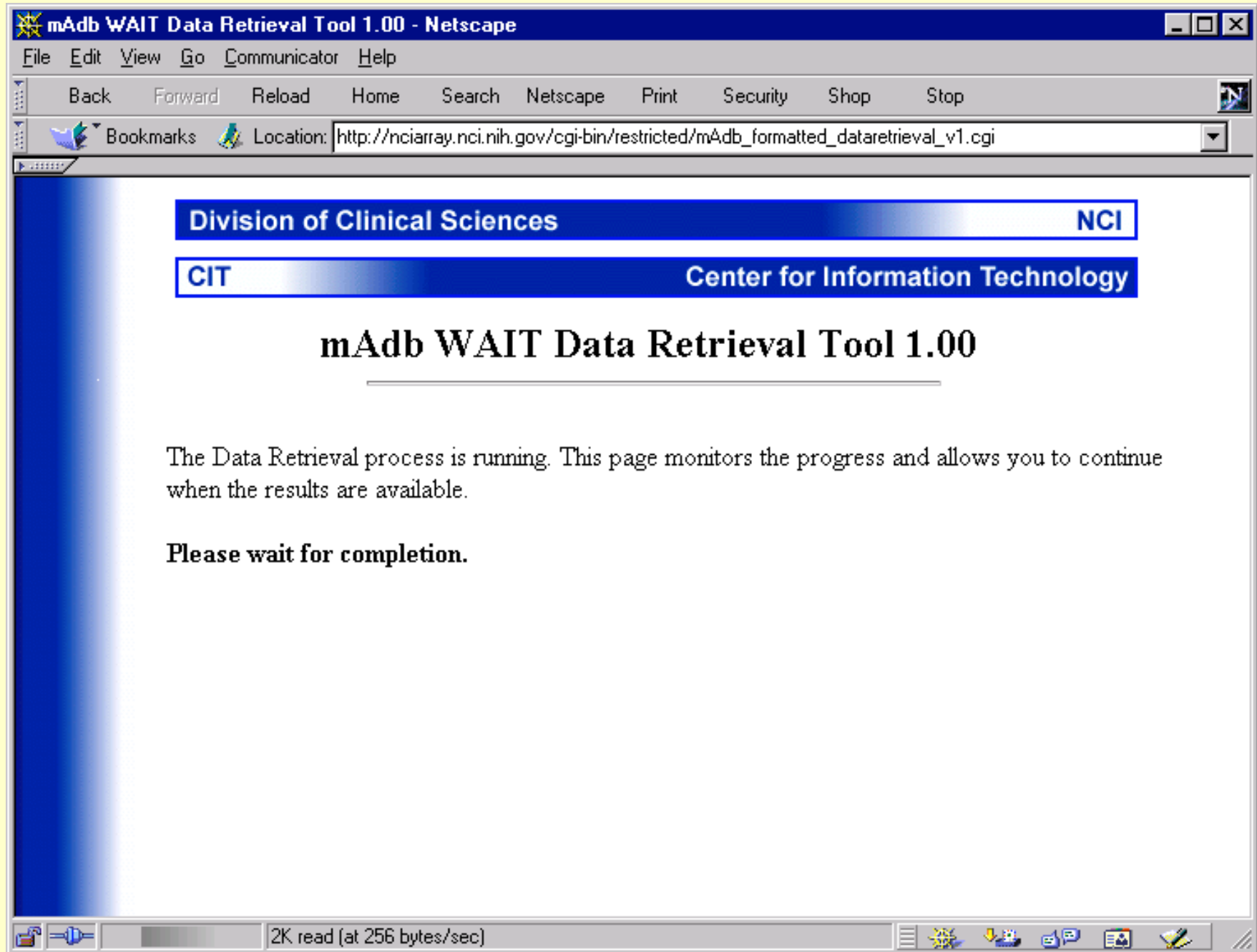
Format Options 

Dataset Formatted for

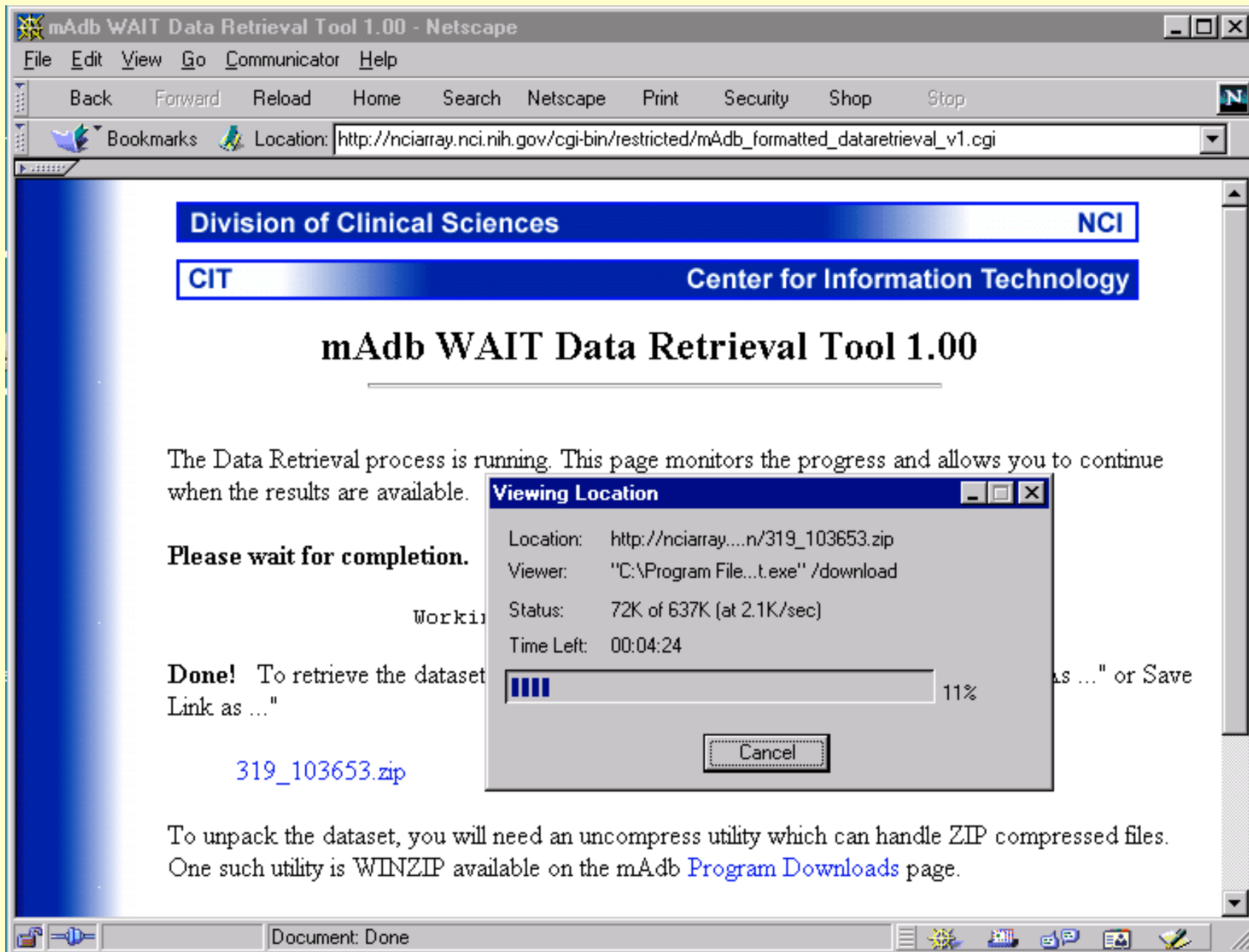
Array Selection 

--	A	Submit
	A	Array Name & Description
<input type="radio"/>	<input checked="" type="radio"/>	MmOC8p6-46 4 Hrs A
<input type="radio"/>	<input checked="" type="radio"/>	MmOC8p6-47 4 Hrs B
<input type="radio"/>	<input checked="" type="radio"/>	MmOC8p6-48 8 Hrs A
<input type="radio"/>	<input checked="" type="radio"/>	MmOC8p6-49 8 Hrs B

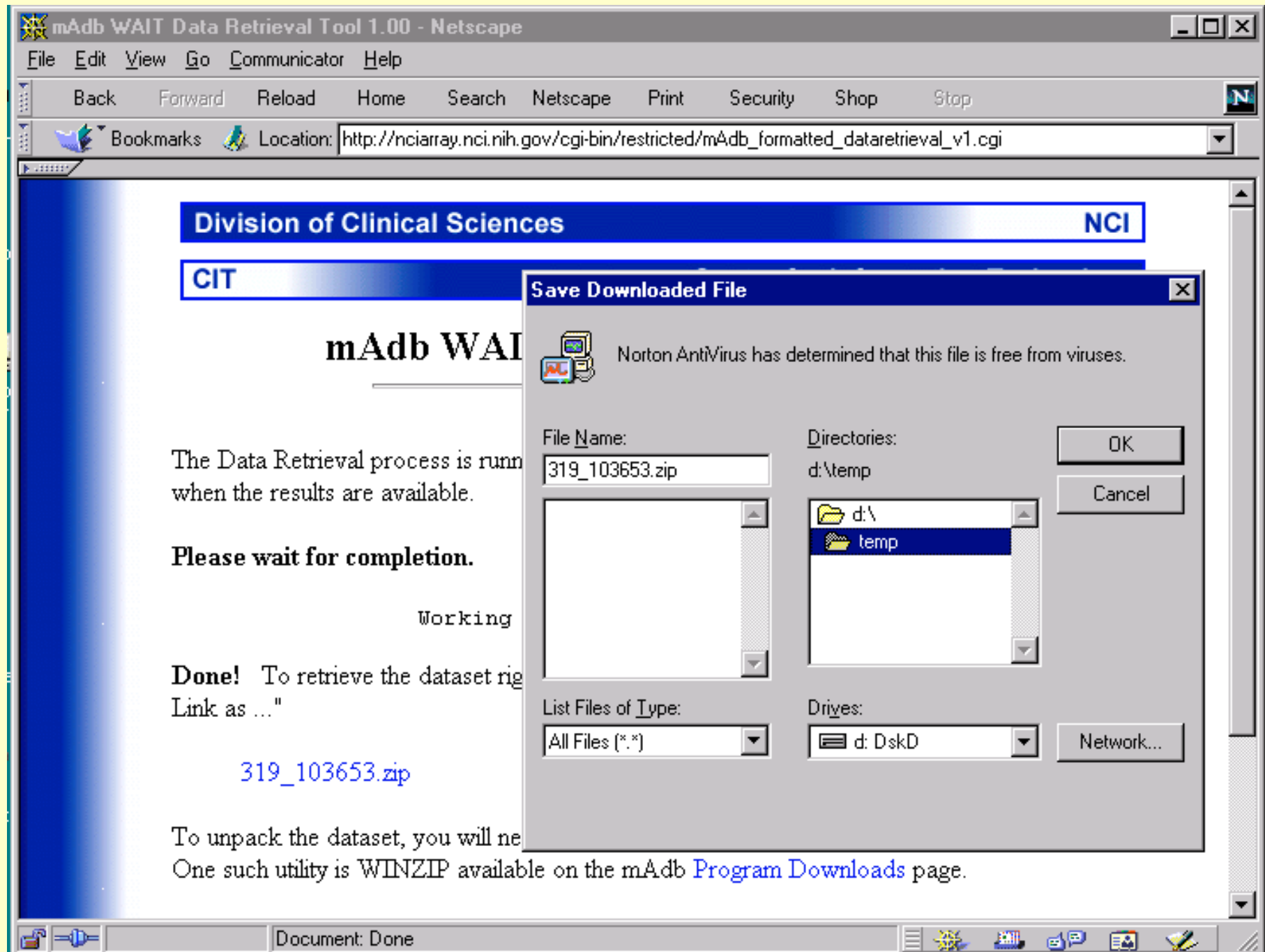
2.5 It will contact the mAdb server to get data



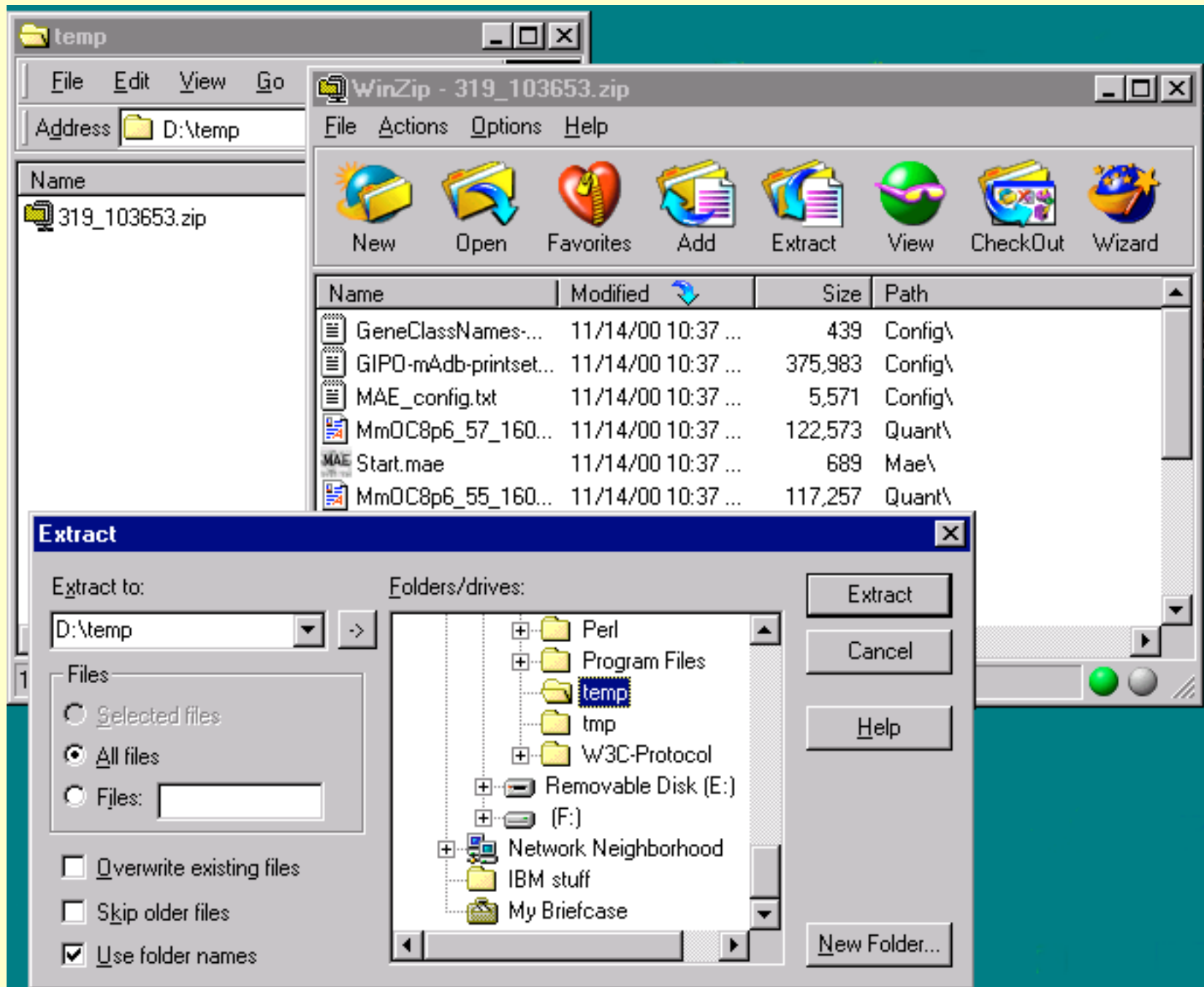
2.6 Click on Zip file (e.g. [319-103653.zip](#)) result to download to your computer.



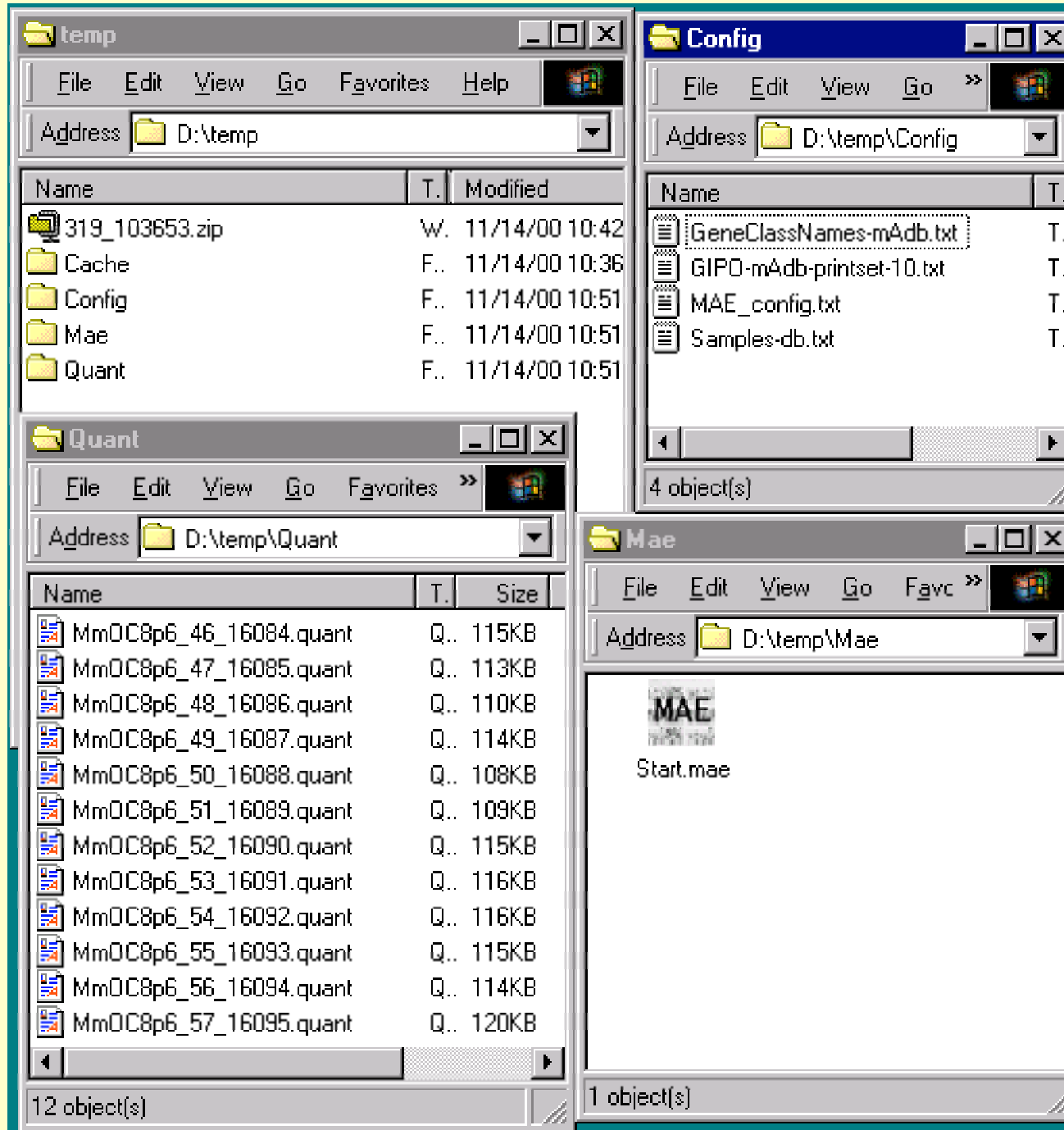
2.7 Save the Zip data file on your local disk



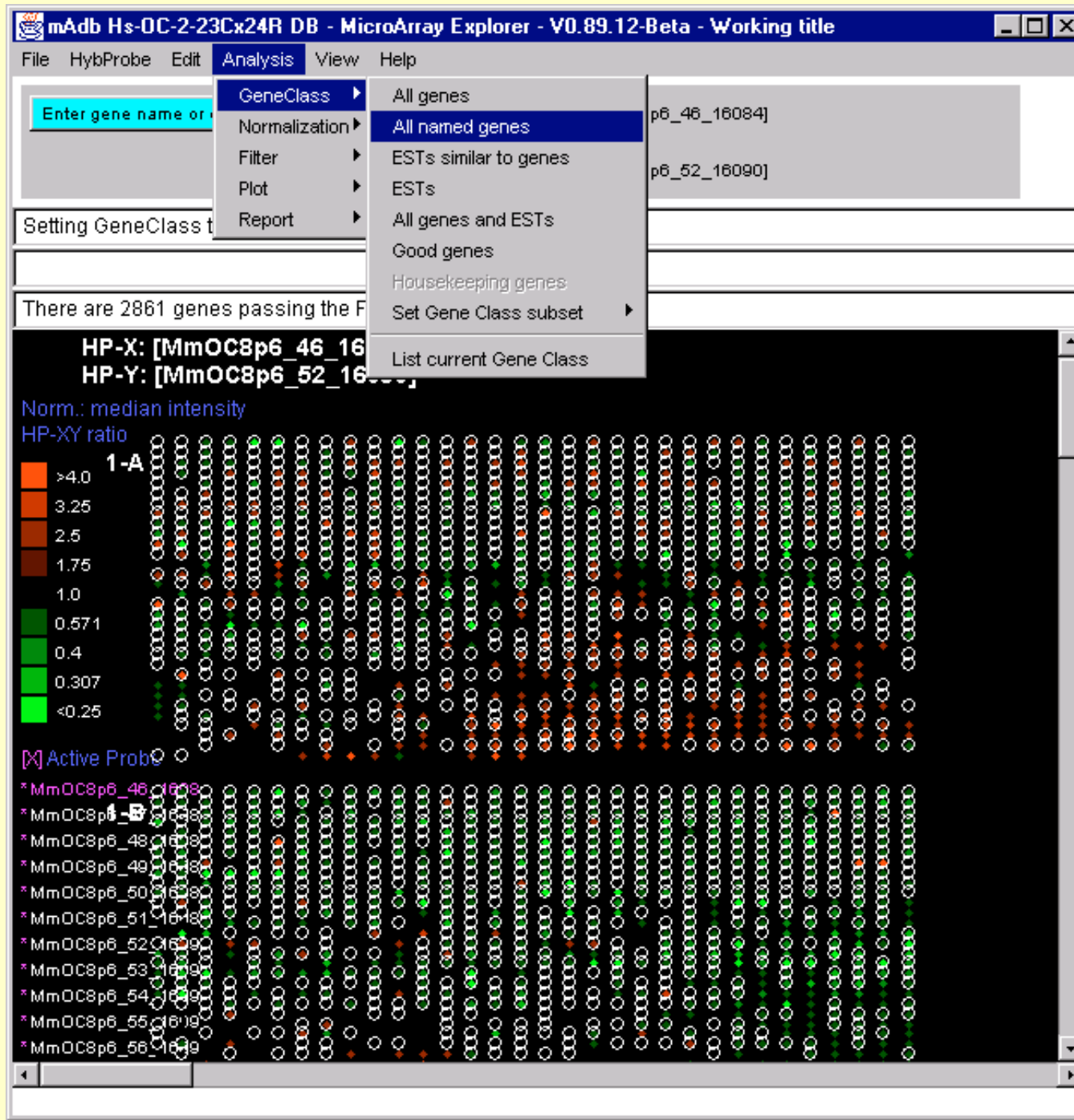
2.8 Unzipping the Zip data file



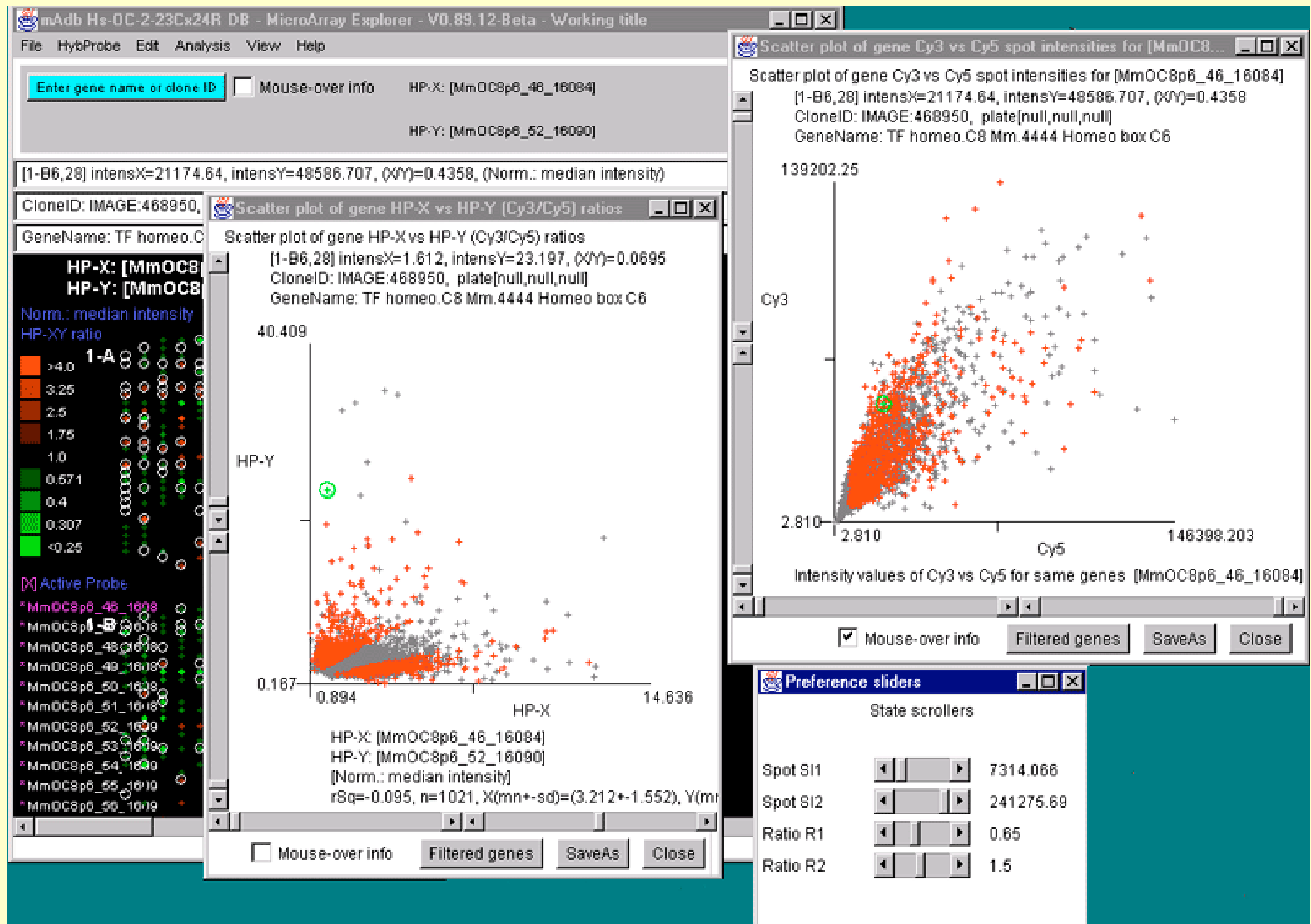
2.9 Inspecting the unzipped data files



2.10 Click on “Start.mae” to start MAExplorer



2.11 Explore data using data filters, plots, etc.



Analysis of mAdb data using MAExplorer

- MAExplorer is fully documented on its Web site,
<http://www.lecb.ncifcrf.gov/MAExplorer>
including the following:
 1. Detailed hyperlinked reference manual with screen shots of all menu operations **<http://www.lecb.ncifcrf.gov/MAExplorer/maeHelp.html>**
 2. Overview - [slide show](#)
 3. Examples of various analysis operations - [slide-show](#)
 4. Short tutorial - showing enough of the fundamental concepts to get started
 5. Advanced tutorial - showing more advanced concepts
 6. Demonstration databases from the MGAP (Mammary Genome Anatomy Program) included in the MAExplorer installation download